#8

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        RAW SEQUENCE LISTING              DATE: 04/30/2001
        PATENT APPLICATION:  US/09/403,269    TIME: 13:57:00

           Input Set : A:\Pto.amc
           Output Set: N:\CRF3\04302001\I403269.raw

    3  <110> APPLICANT: ULF, Lindahl
    4         LI, Jin-Ping
    6  <120> TITLE OF INVENTION: DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a
    7         Process for Its Production
    9  <130> FILE REFERENCE: 003300-589
   11  <140> CURRENT APPLICATION NUMBER: US 09/403,269
   12  <141> CURRENT FILING DATE: 1999-10-18
   14  <150> PRIOR APPLICATION NUMBER: SE 9701454-2
   15  <151> PRIOR FILING DATE: 1997-04-18
   17  <150> PRIOR APPLICATION NUMBER: PCT/SE98/00703
   18  <151> PRIOR FILING DATE: 1998-04-17
   20  <160> NUMBER OF SEQ ID NOS: 13
   22  <170> SOFTWARE: PatentIn version 3.0
   25  <210> SEQ ID NO: 1
   26  <211> LENGTH: 17
   27  <212> TYPE: DNA
   28  <213> ORGANISM: Human
   30  <400> SEQUENCE: 1
   31  gctgattctt ttctgtc                                            17

   34  <210> SEQ ID NO: 2
   35  <211> LENGTH: 13
   36  <212> TYPE: PRT
   37  <213> ORGANISM: Human
   39  <220> FEATURE:
   40  <221> NAME/KEY: PEPTIDE
   41  <222> LOCATION: (5)..(5)
   42  <223> OTHER INFORMATION: Amino acid 5 is Xaa wherein Xaa = any amino acid.
   44  <400> SEQUENCE: 2
W--> 46  Pro Asn Asp Trp Xaa Val Pro Lys Gly Cys Phe Met Ala
   47  1               5                   10
   49  <210> SEQ ID NO: 3
   50  <211> LENGTH: 11
   51  <212> TYPE: PRT
   52  <213> ORGANISM: Human
   54  <220> FEATURE:
   55  <221> NAME/KEY: PEPTIDE
   56  <222> LOCATION: (2)..(10)
   57  <223> OTHER INFORMATION: Amino acids 2 and 10 are Xaa wherein Xaa = any amino acid.
   59  <400> SEQUENCE: 3
W--> 61  Pro Xaa Asp Trp Thr Val Pro Lys Gly Xaa Phe
   62  1               5                   10
   64  <210> SEQ ID NO: 4
   65  <211> LENGTH: 8
   66  <212> TYPE: PRT
   67  <213> ORGANISM: Human
   69  <220> FEATURE:
   70  <221> NAME/KEY: PEPTIDE
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      71 <222> LOCATION: (4)..(4)
      72 <223> OTHER INFORMATION: Amino acid 4 is Xaa wherein Xaa = any amino acid.
      74 <400> SEQUENCE: 4
W--> 76 Pro Asn Asp Xaa Thr Val Pro Lys
      77 1                    5
      79 <210> SEQ ID NO: 5
      80 <211> LENGTH: 15
      81 <212> TYPE: PRT
      82 <213> ORGANISM: Human
      84 <220> FEATURE:
      85 <221> NAME/KEY: PEPTIDE
      86 <222> LOCATION: (1)..(11)
      87 <223> OTHER INFORMATION: Amino acids 1, 2 and 11 are Xaa wherein Xaa = any amino acid.
      89 <400> SEQUENCE: 5
W--> 91 Xaa Xaa Ile Ala Pro Glu Thr Ser Glu Gly Xaa Ser Leu Gln Leu
      92 1                 5                10                 15
      94 <210> SEQ ID NO: 6
      95 <211> LENGTH: 10
      96 <212> TYPE: PRT
      97 <213> ORGANISM: Human
      99 <400> SEQUENCE: 6
     101 Gly Gly Trp Pro Ile Met Val Thr Arg Lys
     102 1                 5                 10
     104 <210> SEQ ID NO: 7
     105 <211> LENGTH: 8
     106 <212> TYPE: PRT
     107 <213> ORGANISM: Human
     109 <400> SEQUENCE: 7
     111 Phe Leu Ser Glu Gln His Gly Val
     112 1                 5
     114 <210> SEQ ID NO: 8
     115 <211> LENGTH: 36
     116 <212> TYPE: PRT
     117 <213> ORGANISM: Human
     119 <220> FEATURE:
     120 <221> NAME/KEY: PEPTIDE
     121 <222> LOCATION: (30)..(30)
     122 <223> OTHER INFORMATION: Amino acid 30 is Xaa wherein Xaa = any amino acid.
     124 <400> SEQUENCE: 8
     126 Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile Tyr Asp
     127 1                 5                10                 15
W--> 129 Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Xaa Trp Asp
     130              20                 25                 30
     132 Tyr His Thr Thr
     133          35
     135 <210> SEQ ID NO: 9
     136 <211> LENGTH: 25
     137 <212> TYPE: DNA
     138 <213> ORGANISM: Human
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W--> 139 <220> FEATURE:
     140 <221> NAME/KEY: misc_feature
     141 <222> LOCATION: (14)..(23)
     142 <223> OTHER INFORMATION: Nucleotides 14, 20 and 23 are "n" wherein "n" = any
     143       nucleotide.
     145 <400> SEQUENCE: 9
W--> 146 ccgaattcaa rgcnatgytn ccnyt                                    25
     149 <210> SEQ ID NO: 10
     150 <211> LENGTH: 26
     151 <212> TYPE: DNA
     152 <213> ORGANISM: Human
     154 <220> FEATURE:
     155 <221> NAME/KEY: misc_feature
     156 <222> LOCATION: (14)..(17)
     157 <223> OTHER INFORMATION: Nucleotides 14 and 17 are "n" wherein "n" = any nucleotide.
     159 <400> SEQUENCE: 10
W--> 160 ccgaattcga yytnmgncay ttyatg                                   26
     163 <210> SEQ ID NO: 11
     164 <211> LENGTH: 25
     165 <212> TYPE: DNA
     166 <213> ORGANISM: Human
     168 <220> FEATURE:
     169 <221> NAME/KEY: misc_feature
     170 <222> LOCATION: (11)..(11)
     171 <223> OTHER INFORMATION: Nucleotide 11 is "n" wherein "n" = any nucleotide.
     173 <400> SEQUENCE: 11
W--> 174 ccggatccgt ngtrtgrtar tccca                                    25
     177 <210> SEQ ID NO: 12
     178 <211> LENGTH: 3085
     179 <212> TYPE: DNA
     180 <213> ORGANISM: Human
     182 <220> FEATURE:
     183 <221> NAME/KEY: CDS
     184 <222> LOCATION: (73)..(1404)
     186 <400> SEQUENCE: 12
     187 tccaagctga attctcatag ctattccaaa gtctatgcac agagagcccc ttatcaccct    60
     189 gatggtgtgt tt atg tcc ttt gaa ggc tac aat gtg gaa gtc cga gac aga    111
     190                Met Ser Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg
     191                  1   5                  10
     193 gtc aag tgc ata agt ggg gtt gaa ggt gta cct tta tct aca cag tgg       159
     194 Val Lys Cys Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp
     195     15                  20                  25
     197 gga cct caa ggc tat ttc tac cca atc cag att gca cag tat ggg tta       207
     198 Gly Pro Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu
     199 30                  35                  40                  45
     201 agt cac tac agc aag aat cta act gaa aaa ccc cct cat ata gag gta       255
     202 Ser His Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val
     203                 50                  55                  60
     205 tat gaa aca gca gaa gac agg gac aaa aac agc aag ccc aat gac tgg       303
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206 Tyr Glu Thr Ala Glu Asp Arg Asp Lys Asn Ser Lys Pro Asn Asp Trp
207         65              70              75
209 act gtg ccc aag ggc tgc ttt atg gct agt gtg gct gat aag tca aga    351
210 Thr Val Pro Lys Gly Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg
211         80              85              90
213 ttc acc aat gtt aaa cag ttc att gct cca gaa acc agt gaa ggt gta    399
214 Phe Thr Asn Val Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val
215         95              100             105
217 tcc ttg caa ctg ggg aac aca aaa gat ttt att att tca ttt gac ctc    447
218 Ser Leu Gln Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu
219 110             115             120                     125
221 aag ttc tta aca aat gga agc gtg tct gtg gtt ctg gag acg aca gaa    495
222 Lys Phe Leu Thr Asn Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu
223             130             135             140
225 aag aat cag ctc ttc act gta cat tat gtc tca aat acc cag cta att    543
226 Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile
227             145             150             155
229 gct ttt aaa gaa aga gac ata tac tat ggc atc ggg ccc aga aca tca    591
230 Ala Phe Lys Glu Arg Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser
231         160             165             170
233 tgg agc aca gtt acc cgg gac ctg gtc act gac ctc agg aaa gga gtg    639
234 Trp Ser Thr Val Thr Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val
235         175             180             185
237 ggt ctt tcc aac aca aaa gct gtc aag cca aca aga ata atg ccc aag    687
238 Gly Leu Ser Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys
239 190             195             200                     205
241 aag gtg gtt agg ttg att gcg aaa ggg aag ggc ttc ctt gac aac att    735
242 Lys Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile
243             210             215             220
245 acc atc tct acc aca gcc cac atg gct gcc ttc ttc gct gcc agt gac    783
246 Thr Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp
247             225             230             235
249 tgg ctg gtg agg aac cag gat gag aaa ggc ggc tgg ccg att atg gtg    831
250 Trp Leu Val Arg Asn Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val
251         240             245             250
253 acc cgt aag tta ggg gaa ggc ttc aag tct tta gag cca ggg tgg tac    879
254 Thr Arg Lys Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr
255         255             260             265
257 tcc gcc atg gcc caa ggg caa gcc att tct aca tta gtc agg gcc tat    927
258 Ser Ala Met Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr
259 270             275             280                     285
261 ctc tta aca aaa gac cat ata ttc ctc aat tca gct tta agg gca aca    975
262 Leu Leu Thr Lys Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr
263             290             295             300
265 gcc cct tac aag ttt ctg tca gag cag cat gga gtc aag gct gtg ttt    1023
266 Ala Pro Tyr Lys Phe Leu Ser Glu Gln His Gly Val Lys Ala Val Phe
267             305             310             315
269 atg aat aaa cat gac tgg tat gaa gaa tat cca act aca cct agc tct    1071
270 Met Asn Lys His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser
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271        320                 325                 330
273 ttt gtt tta aat ggc ttt atg tat tct tta att ggg ctg tat gac tta    1119
274 Phe Val Leu Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu
275        335                 340                 345
277 aaa gaa act gca ggg gaa aaa ctc ggg aaa gaa gcg agg tcc ttg tat    1167
278 Lys Glu Thr Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr
279 350                 355                 360                 365
281 gag cgt ggc atg gaa tcc ctt aaa gcc atg ctc ccc ttg tac gac act    1215
282 Glu Arg Gly Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr
283            370                 375                 380
285 ggc tca gga acc atc tat gac ctc cgg cac ttc atg ctt ggc att gcc    1263
286 Gly Ser Gly Thr Ile Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala
287        385                 390                 395
289 ccc aac ctg gcc cgc tgg gac tat cac acc acc cac atc aat caa ctg    1311
290 Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu
291        400                 405                 410
293 cag ctg ctt agc acc att gat gag tcc cca atc ttc aaa gaa ttt gtc    1359
294 Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val
295    415                 420                 425
297 aag agg tgg aag agc tac ctt aaa ggc agc cgg gca aag cac aac        1404
298 Lys Arg Trp Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys His Asn
299 430                 435                 440
301 tagagctcag aaccaaaatc ctacgtcagc ctctgctgta cacagaaact agaggctctg    1464
303 tgtcagcaga gcataggcac attttaaaag gctgtatact aggttttttgt ggattacatc    1524
305 aaagtgataa atgatcctta aaaccagtct tctgagataa ttgcattcca tgggtttagt    1584
307 gtttagaatg tcgatggcat ttatagcaga aaagtgttta gtcagtgggc tgaatgaaga    1644
309 tgtttaactt ggcctcgctt atcaccctgt tcagttccac aggtagtcca gttctctcga    1704
311 tttgggaaag acaatggtaa gtagctcttg atggccagct gtccagcact tgtctgaaaa    1764
313 cttagtatgg ggctctttta aaatgtggtt atttatgttt atgttgaaag cagactttaa    1824
315 aaaaataatg tgctaaaata cagtaaatat gtacttgtag cctgatagtg actgtgtgca    1884
317 actttaaaaa tgattttttct tttctataaa ttaattttctt agggtggat gagcatttgt    1944
319 tgtgtttgtt caagttgtta tatatgagya atattttgaa tttatgtttt gcttgaagtg    2004
321 tataaattaa aaacacaacc agtgttcagg cttcacagtt atataatgta agcacaacta    2064
323 aaatgaaact tgttgactgc acaagaaatt acaaaacaga acaaaaatgt tatctgttttt    2124
325 atgaaactat ctacaatcag taaagatttg ataatcagta taccctcct gtaccccat    2184
327 tgtggtggtt tcttttttgcc actatctcaa attttgtatt tcatttcaga ctacacttga    2244
329 gagttttgtc tattttggggg ggacatttg gggacatttg ggaaattta ctataaacct    2304
331 agatttgatg aggaggtagt aagtttaata agcccactac cactgccttt tctagattct    2364
333 tttccccttt aaggaaaaat attaggtcag atattataag gattgtagca gatttttttc    2424
335 ctacttagat cattcttggt ctacagcttt ccaaactatt gatgtacaca aaatacatag    2484
337 tttttgtgta agctttcaaa ctttttctggt gttttttctt tgcagttttt aatttttaaat    2544
339 tatttcagct cttggataaa agtgatgcta ctatattagc tgtacatgtg taatcagacc    2604
341 tttattttgg ttttatatcc cacatacctc acataaatag gcatcatagc cctcacaccc    2664
343 tgggcagtgt ctgctctagg acttaggcag taggtcagaa ctgagggagg ttgattttgc    2724
345 tgtctctgtt ttagtgtatg acaatacagt aaatcaatac aataacttat acagattgga    2784
347 aatacgagat ccggtacttt cagaggactg agtctgacac acgcagtgca gtgtgtgtgt    2844
349 gacctgtatg aaatgcacat caagagcgag gtggcacctg cctgccactg catcttgcct    2904
351 ggacttagtc taccaacacc actcagaaat ggcaaaatgc atacatgcct ttgagcaaca    2964
353 tatatgttgt atcagcagcc ggaacgaaga cctacaactg acatgaaact gttagtcact    3024
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                    Input Set : A:\Pto.amc
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L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:139 M:283 W: Missing Blank Line separator, <220> field identifier
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
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